



SEQUENCE LISTING

<110> SHERMAN, LINDA A.
LUSTGARTEN, JOSEPH

<120> RECOMBINANT CONSTRUCTS ENCODING T CELL RECEPTORS
SPECIFIC FOR HUMAN HLA-RESTRICTED TUMOR ANTIGENS

<130> 48340/55793-DIV

<140> 09/774,681

<141> 2001-02-01

<150> 08/812,393

<151> 1997-03-05

<150> 60/012,845

<151> 1996-03-05

<160> 64

<170> PatentIn Ver. 2.1

<210> 1

<211> 1350

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(1332)

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<223> Description of Artificial Sequence: Synthetic
single chain TCR derivative nucleotide sequence

<400> 1

ctc	gag	atg	cag	agg	aac	ctg	gga	gct	gtg	ctg	ggg	att	ctg	tgg	gtg	48
Leu	Glu	Met	Gln	Arg	Asn	Leu	Gly	Ala	Val	Leu	Gly	Ile	Leu	Trp	Val	
1				5					10					15		
cag	att	tgc	tgg	ctg	aaa	gaa	cag	caa	gtg	cag	cag	agt	ccc	gca	tcc	96
Gln	Ile	Cys	Trp	Leu	Lys	Glu	Gln	Gln	Val	Gln	Gln	Ser	Pro	Ala	Ser	
			20					25					30			
ttg	gtt	ctg	cag	gag	ggg	gag	aac	gca	gag	ctc	cag	tgt	agc	ttt	tcc	144
Leu	Val	Leu	Gln	Glu	Gly	Glu	Asn	Ala	Glu	Leu	Gln	Cys	Ser	Phe	Ser	
		35				40						45				
atc	ttt	aca	aac	cag	gtg	cag	tgg	ttt	tac	caa	cgt	cct	ggg	gga	aga	192
Ile	Phe	Thr	Asn	Gln	Val	Gln	Trp	Phe	Tyr	Gln	Arg	Pro	Gly	Gly	Arg	
	50					55				60						
ctc	gtc	agc	ctg	ttg	tac	aat	cct	tct	ggg	aca	aag	cag	agt	ggg	aga	240
Leu	Val	Ser	Leu	Leu	Tyr	Asn	Pro	Ser	Gly	Thr	Lys	Gln	Ser	Gly	Arg	
65					70					75					80	

ctg aca tcc aca aca gtc att aaa gaa cgt cgc agc tct ttg cac att	288
Leu Thr Ser Thr Thr Val Ile Lys Glu Arg Arg Ser Ser Leu His Ile	
85 90 95	
tcc tcc tcc cag atc aca gac tca ggc act tat ctc tgt gcc tca aat	336
Ser Ser Ser Gln Ile Thr Asp Ser Gly Thr Tyr Leu Cys Ala Ser Asn	
100 105 110	
tct gga gga agc aat gca aag cta acc ttc ggg aaa ggc act aaa ctc	384
Ser Gly Gly Ser Asn Ala Lys Leu Thr Phe Gly Lys Gly Thr Lys Leu	
115 120 125	
tct gtt aaa tca ggt ggc gga ggg tct ggc ggg ggt gga tcc ggg ggt	432
Ser Val Lys Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly	
130 135 140	
gga ggc tca gag gct gca gtc acc caa agc cca aga aac aag gtg gca	480
Gly Gly Ser Glu Ala Ala Val Thr Gln Ser Pro Arg Asn Lys Val Ala	
145 150 155 160	
gta aca gga gga aag gtg aca ttg agc tgt aat cag act aat aac cac	528
Val Thr Gly Gly Lys Val Thr Leu Ser Cys Asn Gln Thr Asn Asn His	
165 170 175	
aac aac atg tac tgg tat cgg cag gac acg ggg cat ggg ctg agg ctg	576
Asn Asn Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu	
180 185 190	
atc cat tat tca tat ggt gct ggc agc act gag aaa gga gat atc cct	624
Ile His Tyr Ser Tyr Gly Ala Gly Ser Thr Glu Lys Gly Asp Ile Pro	
195 200 205	
gat gga tac aag gcc tcc aga cca agc caa gag aac ttc tcc ctc att	672
Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile	
210 215 220	
ctg gag ttg gct acc ccc tct cag aca tca gtg tac ttc tgt gcc agc	720
Leu Glu Leu Ala Thr Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser	
225 230 235 240	
ggt gag aca ggg acc aac gaa aga tta ttt ttc ggt cat gga acc aag	768
Gly Glu Thr Gly Thr Asn Glu Arg Leu Phe Phe Gly His Gly Thr Lys	
245 250 255	
ctg tct gtc ctg act agt aac tcc atc atg tac ttc agc cac ttc gtg	816
Leu Ser Val Leu Thr Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val	
260 265 270	
ccg gtc ttc ctg cca gcg aag ccc acc acg acg cca gcg ccg cga cca	864
Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro	
275 280 285	
cca aca ccg gcg ccc acc atc gcg tcg cag ccc ctg tcc ctg cgc cca	912
Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro	
290 295 300	

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tct agt tct aga gat ccc aaa ctc tgc tac ctg ctg gat gga atc ctc 960
Ser Ser Ser Arg Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu
305 310 315 320

ttc atc tat ggt gtc att ctc act gcc ttg ttc ctg aga gtg aag ttc 1008
Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe
325 330 335

agc agg agc gca gac gcc ccc gcg tac cag cag ggc cag aac cag ctc 1056
Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
340 345 350

tat aac gag ctc aat cta gga cga aga gag gag tac gat gtt ttg gac 1104
Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
355 360 365

aag aga cgt ggc cgg gac cct gag atg ggg gga aag ccg aga agg aag 1152
Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
370 375 380

aac cct cag gaa ggc ctg tac aat gaa ctg cag aaa gat aag atg gcg 1200
Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
385 390 395 400

gag gcc tac agt gag att ggg atg aaa ggc gag cgc cgg agg ggc aag 1248
Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
405 410 415

ggg cac gat ggc ctt tac cag ggt ctc agt aca gcc acc aag gac acc 1296
Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
420 425 430

tac gac gcc ctt cac atg cag gcc ctg ccc cct cgc taa gcg gcc gcc 1344
Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
435 440

acc gcg 1350

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<210> 2

<211> 444

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
single chain TCR protein

<400> 2

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Leu Glu Met Gln Arg Asn Leu Gly Ala Val Leu Gly Ile Leu Trp Val
1 5 10 15

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Gln Ile Cys Trp Leu Lys Glu Gln Gln Val Gln Gln Ser Pro Ala Ser
20 25 30

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Leu Val Leu Gln Glu Gly Glu Asn Ala Glu Leu Gln Cys Ser Phe Ser
35 40 45

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Ile Phe Thr Asn Gln Val Gln Trp Phe Tyr Gln Arg Pro Gly Gly Arg
 50 55 60
 Leu Val Ser Leu Leu Tyr Asn Pro Ser Gly Thr Lys Gln Ser Gly Arg
 65 70 75 80
 Leu Thr Ser Thr Thr Val Ile Lys Glu Arg Arg Ser Ser Leu His Ile
 85 90 95
 Ser Ser Ser Gln Ile Thr Asp Ser Gly Thr Tyr Leu Cys Ala Ser Asn
 100 105 110
 Ser Gly Gly Ser Asn Ala Lys Leu Thr Phe Gly Lys Gly Thr Lys Leu
 115 120 125
 Ser Val Lys Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 130 135 140
 Gly Gly Ser Glu Ala Ala Val Thr Gln Ser Pro Arg Asn Lys Val Ala
 145 150 155 160
 Val Thr Gly Gly Lys Val Thr Leu Ser Cys Asn Gln Thr Asn Asn His
 165 170 175
 Asn Asn Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu
 180 185 190
 Ile His Tyr Ser Tyr Gly Ala Gly Ser Thr Glu Lys Gly Asp Ile Pro
 195 200 205
 Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile
 210 215 220
 Leu Glu Leu Ala Thr Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser
 225 230 235 240
 Gly Glu Thr Gly Thr Asn Glu Arg Leu Phe Phe Gly His Gly Thr Lys
 245 250 255
 Leu Ser Val Leu Thr Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val
 260 265 270
 Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro
 275 280 285
 Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
 290 295 300
 Ser Ser Ser Arg Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu
 305 310 315 320
 Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe
 325 330 335
 Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
 340 345 350

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
 355 360 365

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
 370 375 380

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
 385 390 395 400

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
 405 410 415

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
 420 425 430

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
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<210> 3

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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24

<210> 4

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 4

tgagacaaag tccccaatct ctgacag

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<210> 5

<211> 26

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 5

ctgcagctgc tcctcaagta ctattc

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<210> 6
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 6
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<210> 7
 <211> 29
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 <223> Description of Artificial Sequence: Primer

<400> 7
 gaagcagcag agggtttgaa gccacatac 29

<210> 8
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 <212> DNA
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 <223> Description of Artificial Sequence: Primer

<400> 8
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<210> 9
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 <223> Description of Artificial Sequence: Primer

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<210> 10
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 <212> DNA
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 <223> Description of Artificial Sequence: Primer

<400> 10
gcgaagaact caccctggac tggtcat

27

<210> 11
<211> 30
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<223> Description of Artificial Sequence: Primer

<400> 11
gagctccaca gacaacaaga ggacgcagca

30

<210> 12
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<223> Description of Artificial Sequence: Primer

<400> 12
gagctgacgac gttccttagt gactgtg

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<210> 13
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<223> Description of Artificial Sequence: Primer

<400> 13
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<210> 14
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<223> Description of Artificial Sequence: Primer

<400> 14
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<210> 15
<211> 28
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<223> Description of Artificial Sequence: Primer

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28

<210> 16

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 16

acctggagag aatcctaagc tcatcat

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<210> 17

<211> 28

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 17

aggtcttggtg tccctgacag tcctgggt

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<210> 18

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 18

caagcaaaca ctgtagtgca gagcccttcc

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<210> 19

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 19

caagacatcc ataactgccc tacag

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<210> 20

<211> 27

<212> DNA
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 <400> 23
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 <210> 24
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<210> 25
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<223> Description of Artificial Sequence: Primer

<400> 25
gtgaaagggc aaggacaaaa agc 23

<210> 26
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<400> 26
gatatgcgaa cagtatctag gc 22

<210> 27
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<210> 28
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<400> 28
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<210> 29
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<400> 29
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<210> 30
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<220>
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<400> 30
 ataaccatga caatatgtac tgg 23

<210> 31
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<220>
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<400> 31
 ataaccacaa caacatgtac tgg 23

<210> 32
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<400> 32
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<210> 33
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<400> 33
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<210> 34
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 <400> 34
 gattatgttt agctacaata ata 23

<210> 35
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 <400> 35
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<210> 36
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 <400> 36
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<210> 37
 <211> 23
 <212> DNA
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 <400> 37
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<210> 38
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 <220>
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 <400> 38
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<210> 39
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<212> DNA
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 <400> 39
 agaaccatct gtaagagtgg aac 23

<210> 40
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 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 40
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<210> 41
 <211> 23
 <212> DNA
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 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 41
 gtagtcctga aaaagggcac act 23

<210> 42
 <211> 22
 <212> DNA
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 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 42
 catctgtcaa agtggcactt ca 22

<210> 43
 <211> 393
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (1)..(393)

<400> 43
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 Met Lys Ser Leu Ser Val Ser Leu Val Val Leu Trp Leu Gln Leu Asn
 1 5 10 15
 tgg gtg cag agc cag cag aag gtg cag cag agc cca gaa tcc ctc agt 96
 Trp Val Gln Ser Gln Gln Lys Val Gln Gln Ser Pro Glu Ser Leu Ser
 20 25 30
 gtc cca gag gga ggc atg gcc tct ctc aac tgc act tca agt gat cgc 144
 Val Pro Glu Gly Gly Met Ala Ser Leu Asn Cys Thr Ser Ser Asp Arg
 35 40 45
 aat ttt cag tat ttc tgg tgg tac aga cag cat tct gga gaa ggc ccc 192
 Asn Phe Gln Tyr Phe Trp Trp Tyr Arg Gln His Ser Gly Glu Gly Pro
 50 55 60
 aaa gca ctg atg tcc atc ttc tct gat ggt gac aag aaa gaa ggc aga 240
 Lys Ala Leu Met Ser Ile Phe Ser Asp Gly Asp Lys Lys Glu Gly Arg
 65 70 75 80
 ttc aca gct cac ctc aat aag gcc agc ctg cat gtt tcc ctg cac atc 288
 Phe Thr Ala His Leu Asn Lys Ala Ser Leu His Val Ser Leu His Ile
 85 90 95
 aga gac tcc cag ccc agt gac tcc gct ctc tac ttc tgt gca gtt atg 336
 Arg Asp Ser Gln Pro Ser Asp Ser Ala Leu Tyr Phe Cys Ala Val Met
 100 105 110
 gat tat aac cag ggg aag ctt atc ttt ggg cag ggt acc aag tta tct 384
 Asp Tyr Asn Gln Gly Lys Leu Ile Phe Gly Gln Gly Thr Lys Leu Ser
 115 120 125
 atc aag ccc 393
 Ile Lys Pro
 130
 <210> 44
 <211> 131
 <212> PRT
 <213> Homo sapiens
 <400> 44
 Met Lys Ser Leu Ser Val Ser Leu Val Val Leu Trp Leu Gln Leu Asn
 1 5 10 15
 Trp Val Gln Ser Gln Gln Lys Val Gln Gln Ser Pro Glu Ser Leu Ser
 20 25 30
 Val Pro Glu Gly Gly Met Ala Ser Leu Asn Cys Thr Ser Ser Asp Arg
 35 40 45
 Asn Phe Gln Tyr Phe Trp Trp Tyr Arg Gln His Ser Gly Glu Gly Pro
 50 55 60

Lys Ala Leu Met Ser Ile Phe Ser Asp Gly Asp Lys Lys Glu Gly Arg
 65 70 75 80
 Phe Thr Ala His Leu Asn Lys Ala Ser Leu His Val Ser Leu His Ile
 85 90 95
 Arg Asp Ser Gln Pro Ser Asp Ser Ala Leu Tyr Phe Cys Ala Val Met
 100 105 110
 Asp Tyr Asn Gln Gly Lys Leu Ile Phe Gly Gln Gly Thr Lys Leu Ser
 115 120 125
 Ile Lys Pro
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<210> 45
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 <213> Homo sapiens

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 <222> (1)..(402)

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 Met Gly Ser Arg Leu Phe Phe Val Val Ile Leu Leu Cys Ala Lys
 1 5 10 15
 cac atg gag gct gca gtc acc caa agt cca aga agc aag gtg gca gta 96
 His Met Glu Ala Ala Val Thr Gln Ser Pro Arg Ser Lys Val Ala Val
 20 25 30
 aca gga gga aag gtg aca ttg agc tgt cac cag act aat aac cat gac 144
 Thr Gly Gly Lys Val Thr Leu Ser Cys His Gln Thr Asn Asn His Asp
 35 40 45
 tat atg tac tgg tat cgg cag gac acg ggg cat ggg ctg agg ctg atc 192
 Tyr Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu Ile
 50 55 60
 cat tac tca tat gtc gct gac agc acg gag aaa gga gat atc cct gat 240
 His Tyr Ser Tyr Val Ala Asp Ser Thr Glu Lys Gly Asp Ile Pro Asp
 65 70 75 80
 ggg tac aag gcc tcc aga cca agc caa gag aat ttc tct ctc att ctg 288
 Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile Leu
 85 90 95
 gag ttg gct tcc ctt tct cag tca gct gta tat ttc tgt gcc agc agc 336
 Glu Leu Ala Ser Leu Ser Gln Ser Ala Val Tyr Phe Cys Ala Ser Ser
 100 105 110

gat ttc gcc ggg aca ggg ggc ttc tat gaa cag tac ttc ggt ccc ggc 384
 Asp Phe Ala Gly Thr Gly Gly Phe Tyr Glu Gln Tyr Phe Gly Pro Gly
 115 120 125

acc agg ctc acg gtt tct 402
 Thr Arg Leu Thr Val Ser
 130

<210> 46
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 46
 Met Gly Ser Arg Leu Phe Phe Val Val Leu Ile Leu Leu Cys Ala Lys
 1 5 10 15
 His Met Glu Ala Ala Val Thr Gln Ser Pro Arg Ser Lys Val Ala Val
 20 25 30
 Thr Gly Gly Lys Val Thr Leu Ser Cys His Gln Thr Asn Asn His Asp
 35 40 45
 Tyr Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu Ile
 50 55 60
 His Tyr Ser Tyr Val Ala Asp Ser Thr Glu Lys Gly Asp Ile Pro Asp
 65 70 75 80
 Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile Leu
 85 90 95
 Glu Leu Ala Ser Leu Ser Gln Ser Ala Val Tyr Phe Cys Ala Ser Ser
 100 105 110
 Asp Phe Ala Gly Thr Gly Gly Phe Tyr Glu Gln Tyr Phe Gly Pro Gly
 115 120 125
 Thr Arg Leu Thr Val Ser
 130

<210> 47
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 47
 Lys Ile Phe Gly Ser Leu Ala Phe Leu
 1 5

<210> 48
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 48
 Thr Leu Gln Gly Leu Gly Ile Ser Trp Leu
 1 5 10

<210> 49
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 49
 Val Met Ala Gly Val Gly Ser Pro Tyr Val
 1 5 10

<210> 50
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 50
 Val Leu Gln Gly Leu Pro Arg Glu Tyr Val
 1 5 10

<210> 51
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 51
 His Leu Tyr Gln Gly Gln Trp
 1 5

<210> 52
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 52
 Arg Leu Leu Gln Glu Thr Glu Leu Val
 1 5

<210> 53
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 53
 Lys Ile Pro Val Ala Ile Lys Val Leu
 1 5

<210> 54
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 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 54
 Cys Leu Thr Ser Thr Val Gln Leu Val
 1 5

<210> 55
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 55
 Gln Leu Met Pro Tyr Gly Cys Leu Leu
 1 5

<210> 56
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 56
 Val Leu Val Lys Ser Pro Asn His Val
 1 5

<210> 57
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 57
 Asp Ile Asp Glu Thr Glu Tyr His Ala
 1 5

<210> 58
 <211> 9
 <212> PRT
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<210> 59
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<220>
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 peptide

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<220>
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 peptide

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 peptide

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<220>
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 peptide

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<210> 63
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 peptide

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<211> 9

<212> PRT

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<223> Description of Artificial Sequence: Synthetic
peptide

<400> 64

Lys Leu Val Gly Lys Leu Asn Trp Ala
1 5